

Amendments to the Claims

Listing of Claims

- 32. (Previously Presented)** A method comprising steps of:
providing a DNA polymerase having an amino acid sequence that shows at least 30% overall identity with that of SEQ ID NO:4, and further includes a 15 amino-acid motif that is identical to one of SEQ ID NOs 5-22 except that it contains up to 3 amino acid substitutions as compared with the SEQ ID NO;
contacting the DNA polymerase with a template, a primer that binds to the template, and a collection of nucleotides including at least one acyclonucleotide; and
incubating the DNA polymerase with the template and the nucleotides so that the DNA polymerase extends the primer by incorporating the nucleotides.
- 33. (Previously Presented)** The method of claim 32, wherein the DNA polymerase has an amino acid sequence that shows at least 70% overall identity with that of SEQ ID NO:4.
- 34. (Previously Presented)** The method of claim 32 or claim 33, wherein the 15 amino-acid motif is identical to one of SEQ ID NOs 5-22.
- 35. (Previously Presented)** The method of claim 32 or claim 33, wherein the 15 amino-acid motif is identical to one of SEQ ID NOs 5-17 except that it contains up to 3 amino acid substitutions as compared with the SEQ ID NO.
- 36. (Previously Presented)** The method of claim 35, wherein the 15 amino acid motif is identical to one of SEQ ID NOs 5-17.
- 37. (Previously Presented)** The method of claim 32 or 33, wherein the 15 amino acid motif is identical to one of SEQ ID NOs 5-8 except that it contains up to 3 amino acid substitutions as compared with the SEQ ID NO.

38. (Previously Presented) The method of claim 37, wherein the 15 amino acid motif is identical to one of SEQ ID NOs 5-8.

39. (Previously Presented) The method of claim 32 or 33, wherein the step of incubating comprises incubating the DNA polymerase with the template and the nucleotides so that the DNA polymerase extends the primer by incorporating the nucleotides, and preferentially incorporates acyclonucleotides.

40. (Previously Presented) The method of claim 32 or 33, wherein the 15 amino acid motif has up to one amino acid substitution as compared with one of SEQ ID NOs 5-22.

41. (Previously Presented) The method of claim 35, wherein the 15 amino acid motif has up to one amino acid substitution as compared with one of SEQ ID NOs 5-17.

42. (Previously Presented) The method of claim 37, wherein the 15 amino acid motif has up to one amino acid substitution as compared with one of SEQ ID NOs 5-8.

43. (Previously Presented) The method of claim 32 or 33 wherein the DNA polymerase is VentTM, Deep VentTM, 9°N, *Pfu*, VentTM/488L, or 9°N/485L.